



#10

SEQUENCE LISTING

<110> Liu, et al.

<120> Screens and Assays for Agents Useful in Controlling
Parasitic Nematodes

<130> 2002630-0012

<140> 10/051,644

<141> 2002-01-18

<160> 8

<170> PatentIn Ver. 2.1

<210> 1

<211> 425

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Amino Acid
Sequence

<400> 1

Met Ala Val Leu Ala Val Val Leu Leu Leu Ala Cys Leu Glu Arg Ala
1 5 10 15Val Ala Gln Thr Phe Gly Cys Ser Asn Thr Lys Ile Asn Asp Gln Ala
20 25 30Arg Lys Met Phe Tyr Asp Ala His Asn Asp Ala Arg Arg Ser Met Ala
35 40 45Lys Gly Leu Glu Pro Asn Lys Cys Gly Leu Leu Ser Gly Gly Lys Asn
50 55 60Val Tyr Glu Leu Asn Trp Asp Cys Glu Met Glu Ala Lys Ala Gln Glu
65 70 75 80Trp Ala Asp Gly Cys Pro Ser Ser Phe Gln Thr Phe Asp Pro Thr Trp
85 90 95Gly Gln Asn Tyr Ala Thr Tyr Met Gly Ser Ile Ala Asp Pro Leu Pro
100 105 110

Tyr Ala Ser Met Ala Val Asn Gly Trp Trp Ser Glu Ile Arg Thr Val

	115		120		125	
Gly	Leu Thr Asp Pro Asp Asn Lys Tyr Thr Asn Ser Ala Met Phe Arg					
130		135		140		
Phe Ala Asn Met Ala Asn Gly Lys Ala Ser Ala Phe Gly Cys Ala Tyr						
145		150		155		160
Ala Leu Cys Ala Gly Lys Leu Ser Ile Asn Cys Ile Tyr Asn Lys Ile						
	165		170		175	
Gly Tyr Met Thr Asn Ala Ile Ile Tyr Glu Lys Gly Asp Ala Cys Thr						
	180		185		190	
Ser Asp Ala Glu Cys Thr Thr Tyr Ser Asp Ser Gln Cys Lys Asn Gly						
	195		200		205	
Leu Cys Tyr Lys Ala Pro Gln Ala Pro Val Val Glu Thr Phe Thr Met						
	210		215		220	
Cys Pro Ser Val Thr Asp Gln Ser Asp Gln Ala Arg Gln Asn Phe Leu						
225		230		235		240
Asp Thr His Asn Lys Leu Arg Thr Ser Leu Ala Lys Gly Leu Glu Ala						
	245		250		255	
Asp Gly Ile Ala Ala Gly Ala Phe Ala Pro Met Ala Lys Gln Met Pro						
	260		265		270	
Lys Leu Val Lys Tyr Ser Cys Thr Val Glu Ala Asn Ala Arg Thr Trp						
	275		280		285	
Ala Lys Gly Cys Leu Tyr Gln His Ser Thr Ser Ala Gln Arg Pro Gly						
	290		295		300	
Leu Gly Glu Asn Leu Tyr Met Ile Ser Ile Asn Asn Met Pro Lys Ile						
305		310		315		320
Gln Thr Ala Glu Asp Ser Ser Lys Ala Trp Trp Ser Glu Leu Lys Asp						
	325		330		335	
Phe Gly Val Gly Ser Asp Asn Ile Leu Thr Gln Ala Val Phe Asp Arg						
	340		345		350	
Gly Val Gly His Tyr Thr Gln Met Ala Trp Glu Gly Thr Thr Glu Ile						
	355		360		365	
Gly Cys Phe Val Glu Asn Cys Pro Thr Phe Thr Tyr Ser Val Cys Gln						

370

375

380

Tyr Gly Pro Ala Gly Asn Tyr Met Asn Gln Leu Ile Tyr Thr Lys Gly
 385 390 395 400

Ser Pro Cys Thr Ala Asp Ala Asp Cys Pro Gly Thr Gln Thr Cys Ser
 405 410 415

Val Ala Glu Ala Leu Cys Val Ile Pro
 420 425

<210> 2

<211> 1341

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:cDNA Nucleotide
 Sequence

<400> 2

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aatgatgcaa gacgaagcat ggctaaaggg cttgagccaa acaagtgcgg actcttatct 180
ggtggaaaga atgtttatga attgaattgg gattgcgaga tggaagcaaa agctcaggaa 240
tgggcagacg gatgtcccag ctctttccag acatttgatc caacatgggg gcagaactac 300
gcgacgtaca tgggatcgat tgctgatccg ctccatacg cttccatggc tgттаатggg 360
tggtggtcgg aaattagaac cgtaggactt acggatcctg ataacaagta cactaacagt 420
gcaatgttcc gatttgctaa tatggcaaat ggtaaagctt cagcttttgg atgtgcatac 480
gcgttggtcg caggaaaact atccatcaat tgcatttaca acaagatagg atacatgacc 540
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gttgaagcaa acgccagaac atgggcaaaa ggatgccttt accagcattc aacaagcgca 900
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1341

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<210> 3

<211> 473

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Amino Acid
Sequence

<400> 3

Met Asn Val Val Leu Ser Ala Val Thr Leu Phe Leu Ile Phe Arg Tyr
1 5 10 15

Ala Gln Thr Val Asn Ile Glu Gly Ser Gly Gly Asn Asp Glu Leu Leu
20 25 30

Glu Gln Asn Val Trp Asn Asp Val Asp Asp Lys Val Val Glu Ala Leu
35 40 45

Gly Gly Leu Asp Asp Glu Leu Leu Thr Glu His Val Cys Asn Lys Ser
50 55 60

Thr Ile Thr Gln Leu Gln Gln Glu Ile Ile Leu Thr Thr His Asn Glu
65 70 75 80

Leu Arg Arg Ser Leu Ala Phe Gly Lys Gln Arg Asn Lys Arg Gly Leu
85 90 95

Met Asn Gly Ala Arg Asn Met Tyr Lys Leu Asp Trp Asp Cys Glu Leu
100 105 110

Ala Ser Leu Ala Ala Asn Trp Ser Thr Ser Cys Pro Gln His Phe Met
115 120 125

Pro Gln Ser Val Leu Gly Ser Asn Ala Gln Leu Phe Lys Arg Phe Tyr
130 135 140

Phe Tyr Phe Asp Gly His Asp Ser Thr Val His Met Arg Asn Ala Met
145 150 155 160

Lys Tyr Trp Trp Gln Gln Gly Glu Glu Lys Gly Asn Glu Asp Gln Lys
165 170 175

Asn Arg Phe Tyr Ala Arg Arg Asn Tyr Phe Gly Trp Ala Asn Met Ala
180 185 190

Lys Gly Lys Thr Tyr Arg Val Gly Cys Ser Tyr Ile Met Cys Gly Asp
195 200 205

Gly Glu Ser Ala Leu Phe Thr Cys Leu Tyr Asn Glu Lys Ala Gln Cys
 210 215 220

Glu Lys Glu Met Ile Tyr Glu Asn Gly Lys Pro Cys Cys Glu Asp Lys
 225 230 235 240

Asp Cys Phe Thr Tyr Pro Gly Ser Lys Cys Leu Val Pro Glu Gly Leu
 245 250 255

Cys Gln Ala Pro Ser Met Val Lys Asp Asp Gly Gly Ser Phe Gln Cys
 260 265 270

Asp Asn Ser Leu Val Ser Asp Val Thr Arg Asn Phe Thr Leu Glu Gln
 275 280 285

His Asn Phe Tyr Arg Ser Arg Leu Ala Lys Gly Phe Glu Trp Asn Gly
 290 295 300

Glu Thr Asn Thr Ser Gln Pro Lys Ala Ser Gln Met Ile Lys Met Glu
 305 310 315 320

Tyr Asp Cys Met Leu Glu Arg Phe Ala Gln Asn Trp Ala Asn Asn Cys
 325 330 335

Val Phe Ala His Ser Ala His Tyr Glu Arg Pro Asn Gln Gly Gln Asn
 340 345 350

Leu Tyr Met Ser Ser Phe Ser Asn Pro Asp Pro Arg Ser Leu Ile His
 355 360 365

Thr Ala Val Glu Lys Trp Trp Gln Glu Leu Glu Glu Phe Gly Thr Pro
 370 375 380

Ile Asp Asn Val Leu Thr Pro Glu Leu Trp Asp Leu Lys Gly Lys Ala
 385 390 395 400

Ile Gly His Tyr Thr Gln Met Ala Trp Asp Arg Thr Tyr Arg Leu Gly
 405 410 415

Cys Gly Ile Ala Asn Cys Pro Lys Met Ser Tyr Val Val Cys His Tyr
 420 425 430

Gly Pro Ala Gly Asn Arg Lys Asn Asn Lys Ile Tyr Glu Ile Gly Asp
 435 440 445

Pro Cys Glu Val Asp Asp Asp Cys Pro Ile Gly Thr Asp Cys Glu Lys
 450 455 460

Thr Thr Ser Leu Cys Val Ile Ser Lys
465 470

<210> 4
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:cDNA Nucleotide
Sequence

<400> 4
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gacgacaagg ttgtagaagc acttggtggt cttgatgatg aactgctaac cgaacatgtg 180
tgtaacaaat caacgatcac tcagctacag caggagatca tcttgacaac ccacaatgaa 240
ttacgaagat cattggcitt cggaaagcaa agaaacaaga gaggtctcat gaacgggtgcg 300
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aagcgtttct atttttattt tgatgggcac gactctactg tacatatgcg aaacgcgatg 480
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tgctcgtata ttatgtgctg cgacgggtgaa tctgcacttt tcaattgtct ttataacgaa 660
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tctatggtaa aggatgatgg aggaagtttc caatgtgata actcccttgt gtcagatgtc 840
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gaatggaatg gagaaacaaa cacttcccag ccaaaggcta gtcaaatgat caaaatggag 960
tatgactgca tgttggaacg gtttgcaaa aactgggcaa ataattgctt tttgacac 1020
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cctgatccta gaagccttat acatacggcc gtcgagaagt ggtggcagga attggaggag 1140
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aactgtccga agatgtcgtg cgtggtttgt cactatgggc cagcaggcaa cagaaagaac 1320
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<210> 5
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Clustal W
Alignment of VAP-1, VAP-2, and Selected Other

Nematode VA Proteins.

<400> 5

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Met Phe Ser Pro Val Ile Val Ser Val Ile Phe Thr Ile Ala Phe Cys
 1             5             10             15

Asp Ala Ser Pro Ala Arg Asp Gly Phe Gly Cys Ser Asn Ser Gly Ile
          20             25             30

Thr Asp Lys Asp Arg Gln Ala Phe Leu Asp Phe His Asn Asn Ala Arg
      35             40             45

Arg Arg Val Ala Lys Gly Val Glu Asp Ser Asn Ser Gly Lys Leu Asn
      50             55             60

Pro Ala Lys Asn Met Tyr Lys Leu Ser Trp Asp Cys Ala Met Glu Gln
65             70             75             80

Gln Leu Glu Asp Ala Ile Gln Ser Cys Pro Ser Ala Phe Ala Gly Ile
          85             90             95

Gln Gly Val Ala Gln Asn Val Met Ser Trp Ser Ser Ser Gly Gly Phe
      100             105             110

Pro Asp Pro Ser Val Lys Ile Glu Gln Thr Leu Ser Gly Trp Trp Ser
      115             120             125

Gly Ala Lys Lys Asn Gly Val Gly Pro Asp Asn Lys Tyr Asn Gly Gly
      130             135             140

Gly Leu Phe Ala Phe Ser Asn Met Val Tyr Ser Glu Thr Thr Lys Leu
      145             150             155             160

Gly Cys Ala Tyr Lys Val Cys Gly Thr Lys Leu Ala Val Ser Cys Ile
          165             170             175

Tyr Asn Gly Val Gly Tyr Ile Thr Asn Gln Pro Met Trp Glu Thr Gly
      180             185             190

Gln Ala Cys Lys Thr Gly Ala Asp Cys Ser Thr Tyr Lys Asn Ser Gly
      195             200             205

Cys Glu Asp Gly Leu Cys Thr Lys Gly Pro
      210             215

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<210> 6

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Clustal W
Alignment of VAP-1, VAP-2, and selected other
nematode VA Proteins.

<400> 6

Asp	Val	Pro	Glu	Thr	Asn	Gln	Gln	Cys	Pro	Ser	Asn	Thr	Gly	Met	Thr
1				5				10					15		
Asp	Ser	Val	Arg	Asp	Thr	Phe	Leu	Val	His	Asn	Glu	Phe	Arg	Ser	Ser
			20				25					30			
Val	Ala	Arg	Gly	Leu	Glu	Pro	Asp	Ala	Leu	Gly	Gly	Asn	Ala	Pro	Lys
		35					40					45			
Ala	Ala	Lys	Met	Leu	Lys	Met	Val	Tyr	Asp	Cys	Glu	Val	Glu	Ala	Ser
	50					55					60				
Ala	Ile	Arg	His	Gly	Asn	Lys	Cys	Val	Tyr	Gln	His	Ser	His	Gly	Glu
65					70				75					80	
Asp	Arg	Pro	Gly	Leu	Gly	Glu	Asn	Ile	Tyr	Lys	Thr	Ser	Val	Leu	Lys
				85					90					95	
Phe	Asp	Lys	Asn	Lys	Ala	Ala	Lys	Gln	Ala	Ser	Gln	Leu	Trp	Trp	Asn
			100					105					110		
Glu	Leu	Lys	Glu	Phe	Gly	Val	Gly	Pro	Ser	Asn	Val	Leu	Thr	Thr	Ala
	115						120					125			
Leu	Trp	Asn	Arg	Pro	Gly	Met	Gln	Ile	Gly	His	Tyr	Thr	Gln	Met	Ala
	130					135					140				
Trp	Asp	Thr	Thr	Tyr	Lys	Leu	Gly	Cys	Ala	Val	Val	Phe	Cys	Asn	Asp
145					150					155				160	
Phe	Thr	Phe	Gly	Val	Cys	Gln	Tyr	Gly	Pro	Gly	Gly	Asn	Tyr	Met	Gly
			165					170						175	
His	Val	Ile	Tyr	Thr	Met	Gly	Gln	Pro	Cys	Ser	Gln	Cys	Ser	Pro	Gly
		180					185						190		
Ala	Thr	Cys	Ser	Val	Thr	Glu	Gly	Leu	Cys	Ser	Ala	Pro			
	195						200					205			

<210> 7

<211> 207

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Clustal W
Alignment of VAP-1, VAP-2, and selected other
nematode VA proteins.

<400> 7

Met	Asn	Tyr	Leu	Leu	Leu	Val	Val	Ala	Leu	Ala	Val	Gly	Cys	Ser	Ala	
1				5					10					15		
Asp	Phe	Gly	Ser	Ser	Gly	Gln	Asn	Gly	Ile	Ile	Asn	Ala	His	Asn	Thr	
			20					25					30			
Leu	Arg	Ser	Lys	Ile	Ala	Lys	Gly	Thr	Tyr	Val	Ala	Lys	Gly	Thr	Gln	
		35					40					45				
Lys	Ser	Pro	Gly	Thr	Asn	Leu	Lys	Met	Lys	Trp	Asp	Ser	Ala	Val		
	50					55				60						
Ala	Ala	Ser	Ala	Gln	Asn	Tyr	Ala	Asn	Gly	Cys	Pro	Thr	Gly	His	Ser	
65					70					75					80	
Gly	Asp	Ala	Gly	Leu	Gly	Glu	Asn	Leu	Tyr	Trp	Tyr	Trp	Thr	Ser	Gly	
			85					90						95		
Ser	Leu	Gly	Asp	Leu	Asn	Gln	Tyr	Gly	Ser	Ala	Ala	Ser	Ala	Ser	Trp	
		100						105					110			
Glu	Lys	Glu	Phe	Gln	Asp	Tyr	Gly	Trp	Lys	Ser	Asn	Leu	Met	Thr	Ile	
	115						120					125				
Asp	Leu	Phe	Asn	Thr	Gly	Ile	Gly	His	Ala	Thr	Gln	Met	Ala	Trp	Ala	
	130					135					140					
Lys	Ser	Asn	Leu	Ile	Gly	Cys	Gly	Val	Lys	Asp	Cys	Gly	Arg	Asp	Ser	
145				150					155					160		
Asn	Gly	Leu	Asn	Lys	Val	Thr	Val	Val	Cys	Gln	Tyr	Lys	Pro	Gln	Gly	
			165					170						175		
Asn	Phe	Ile	Asn	Gln	Tyr	Ile	Tyr	Val	Ser	Gly	Ala	Thr	Cys	Ser	Gly	
		180					185						190			

Cys Pro Ser Gly Thr Ser Cys Glu Thr Ser Thr Gly Leu Cys Val
 195 200 205

<210> 8

<211> 231

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Clustal W
 Alignment of VAP-1, VAP-2, and selected other
 nematode VA proteins.

<400> 8

Met	Ser	Asn	Lys	Leu	Ile	Ile	Ser	Ile	Leu	Ile	Leu	Thr	Ile	Ile	Tyr
1				5					10					15	
Thr	Val	Val	Asn	Ser	Leu	Thr	Val	Pro	Glu	Gln	Asn	Ala	Val	Val	Asp
			20					25					30		
Cys	Ile	Asn	Lys	Tyr	Arg	Ser	Gln	Leu	Ala	Asn	Gly	Lys	Thr	Lys	Asn
		35					40					45			
Lys	Asn	Gly	Gly	Asn	Phe	Pro	Ser	Gly	Lys	Asp	Ile	Leu	Glu	Val	Ser
	50					55					60				
Tyr	Ser	Lys	Asp	Leu	Glu	Lys	Ser	Ala	Gln	Arg	Trp	Ala	Asn	Lys	Cys
65					70					75					80
Ile	Phe	Asp	His	Asn	Gly	Thr	Asp	Leu	Tyr	Ser	Gly	Gly	Lys	Phe	Tyr
			85						90					95	
Gly	Glu	Asn	Leu	Tyr	Leu	Asp	Gly	Asp	Phe	Glu	His	Lys	Asn	Ile	Thr
			100					105					110		
Gln	Leu	Met	Ile	Asp	Ala	Cys	Asn	Ala	Trp	Trp	Gly	Glu	Ser	Thr	Thr
		115						120				125			
Asp	Gly	Val	Pro	Pro	Ser	Trp	Ile	Asn	Asn	Phe	Leu	Pro	Thr	Asp	Asn
		130				135						140			
Lys	Glu	Asn	Asp	Glu	Lys	Phe	Glu	Ala	Val	Gly	His	Trp	Thr	Gln	Met
145					150					155					160
Ala	Trp	Ala	Lys	Thr	Tyr	Gln	Ile	Gly	Cys	Ala	Leu	Lys	Val	Cys	His
				165					170					175	

Lys Pro Asp Cys Asn Gly Asn Leu Ile Asp Cys Arg Tyr Tyr Pro Gly
 180 185 190

Gly Asn Gly Met Gly Ser Pro Ile Tyr Gln Gln Gly Lys Pro Ala Ser
 195 200 205

Gly Cys Gly Lys Ala Gly Pro Ser Thr Lys Tyr Ser Gly Leu Cys Lys
 210 215 220

Pro Asp Pro His Gln Asn Asn
 225 230